WO 98/11228 PCT/GB97/02424

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5	<ul><li>(A) LENGTH: 797 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: unknown</li></ul>	
3	(ii) MOLECULE TYPE: cDNA	
10	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U13	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
15	CGGCACGAGG NAGAACCTTT TGACAGAGTT GTTGTCATGG CAACAAAAGC TTCTCTCTC	60
	ATAAAAGGCT TTGCCTTGCT GGTTTCAGTC CTTGTAGCAG TTCCAACAAG AGTGCAATCG	120
20	ATTGGTGTCT GCTACGGCAT GCTCGGCAAC AATCTTCCCC CGCCCAGCGA GGTGGTCAGT	180
	CTCTACAAAT CCAACAACAT CGCGAGGATG AGACTCTACG ATCCAAACCA AGCCGCCCTG	240
Ti.	CAAGCCCTCA GGAACTCCAA CATCCAAGTC CTGTTGGATG TCCCCCGATC CGACGTGCAG	300
125 U	TCACTGGCCT CCAATCCTTC GGCCGCCGGC GACTGGATCC GGAGGAACGT CGTCGCCTAC	360
i,	TGGCCCAGCG TCTCCTTTCG ATACATAGCT GTCGGAAACG AGCTGATCCC CGGATCGGAT	420
30	CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC	480
	CTGCAAAACC AGATCAAGGT CTCGACCGCG GTCGACACGG GCGTCCTCGG CACGTCCTAC	540
35	CCTCCCTCCG CCGGCGCCTT CTCCTCCGCC GCCCAGGCGT TACCTGANCC CCATCGTGCA	600
	GTTCTTGGCG ANTAACGGAA CGCCGCTCCT GGTCAATGTG TACCTTATTT TAACTACACC	660
eř zk	GGCAACCCGG GANAGATCTC GCTGCCTACN CCCTGTTCAC GGCCNCGGGG TCTCNTGCAG	720
40	GATGGGCGAA TTCCNCTATC ANAANCTGTT CANTCCATCT TCNAAACCGG TCTTCCCGGG	780
	CTGGAAAAA TTGGAAG	797
45	(2) INFORMATION FOR SEQ ID NO: 6:	
13	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 792 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	
50	(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
55	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U136	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
	GGCACGAGGA GAACCCTTTT GACAGAGTTG TTGTCATGGC AACAAAAGCT TCTCTCCA	60
65	TAAAAGGCTT TGCCTTGCTG GTTTCAGTCC TTGTAGCAGT TCCAACAAGA GTGCAATCGA	120
	TTGGTGTCTG CTACGGAATG CTCGGCAACA ATCTTCCCCC GCCCAGCGAG GTGGTCAGTC	180
	TCTACAAATC CAACAACATC GCGAGGATGA GACTCTACGA TCCAAACCAG GCCGCCCTGC	240

AAGCCCTCAG GAACTCCAAC ATCCAAGTCC TGTTGGATGT CCCCCGATCC GACGTGCAGT 300

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	CACTGGCCTC CAATCCTTCG GCCGCCGGCG ACTGGATCCG GAGGGAACGT CGTCGCCTAC	360
	TGGCCCAGCG TCTCCTTTCG ATACATAGCT GTCGGAAACG ANCTGATCCC CGGATCGGAT	420
5	CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC	480
	CTGCAAAACC AGATCAAGGT CTCCGACCGC GGTCGACACG GGCGTCCTCG GCACGTCCTA	540
10	CCCTCCCTCC CGCCGGNGCC TTCTCCTCCG CCGCCCAAGC GTNCTGANCC CCATCGTGCA	600
	NTTCTTTGGC GAAATAACGG ANCGCCGCTC CCNGGTCCAT GTTTTTCCCT TATTTTAACT	660
	ACNCCGGCAA CCCNGGAAAG ATTTCGCTGC CCTTACGCCC CCTGGTTTCC NNGGGGCTTC	720
15	CCGGGCGTTT CTTCCTTTGC CAGGGANTNG GGGCGAATTC CCNNCTTTTC CANAAACCTT	780
	GTTCCAACNC CC	792
20	(2) INFORMATION FOR SEQ ID NO: 7:	
the are find the	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 855 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: unknown	
Straft Sport	(ii) MOLECULE TYPE: cDNA	
30	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U21	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
10 10 10 10 10 10 10 10 10 10 10 10 10 1	CGGCACGAGT CTCTCTGT CTCTCCGTCG TCTCGTTGTC TGTTCGTTAG GGCTTGCGAT .	60
40	CGCCACCGGT CGCGAGGGTT GGAGCCATGG AATTCTTGCG GTTTGGGGCT GAGGTGGCGG	120
	CAGGAGAGGA AGCCGCGACG GGGTACTGGA TGCGATGGCA GACGCTCGTC TGCGCTCTGA	180
	TCGTCGTCGC CCCGGCGGTC GCCGCGGTGG TTGTCGCGGC GCGGGCGCCG GCGCCGGCGC	240
45	GACCGCTCAG GGCCGTCGAT CTCTGGGCGC CGTGCTGGGC CGGGATGCAC CCGGCCTGGC	300
	TTCTCGCGTA CCGCGGCTTC NTGTTCTTGG CCATGGCGTG GCTACTCTTC CANATGATTC	360
50	TGTTTCGCGG ATTCTCCGCG TTCTACTTCT ATACTCAGTG GACGTTTGCC TTAGTCATTG	420
	TCTATTTTGC GATCGCAACC ATTATATCCG CCCATGGCTG CTGGCTTTAC TCAAAGAGAA	480
	GTATTATGCC AGATCAGGAG GTCAACAGAT TCCTAAATGG TGGTTTTGAG CANAATAGTC	540
55	CTATGACTCT ACCTTTGAGG ACCAACAAAA ATATGAATGT TATAAGATTG CAAAGCTATC	600
	NTGAACAGGA NGCTGATGAA NAAAAANCTG GATTTTGGGG TCCTGCTATG CNACTNGTCT	660
60	ATCAAAACCA TTGCANGTGC TGTAATTGTT GAAANACATT GTATTTTGGG NTCNTNCTAA	720
	TACCATATTT GTCTTCTATA AATTTCAGGC TAAATGCTAT AATGGGCTGC ATGCATTCTC	780
	TTAATGCTGT GTTTCTTCNA ATCCAACACT TTTCTCAATA ACCTGCCATT CCCNTNTTTC	840
65	NAATGGCATT TTTGC	855

(2) INFORMATION FOR SEQ ID NO: 8:

65

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 722 base pairs
    (B) TYPE: nucleic acid

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	(C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
5	(ii) MOLECULE TYPE: cDNA	
	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U31	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
	CGGCACGAGA GAGAGAGAG GAGAGAGAGA GAGAGAGA	60
15	GAGAGAGAC CTAGACCGGC ATCNTCGTGC TTGCCGAGGG GCGGCTTATG ANTCTTGGTT	120
	GTGCCACTGG GCATCCCAGC TTCGTCNTGT CCTGCTCCTT CACCANCCAN GTGATNGCAC	180
20	NACTGGANTT ATGGANGGAA ANGGCGACCG GCNNGTACGA NAAGAANGTC TATGTGCTGC	240
## E	CCANGCNTCT GGATGAGAGG GTGGCNGCGC TCCNCCTCGG CAAGCTGGGT GCCNCGCTCA	300
Total Bull State of the State o	CCNAGCTTAC NCCNTCGCGG GCTGATTACA TTAGCGTCCC GATCGAGGGA CCCTACANGC	. 360
(12)	CTGCTCACTA CNGGTATTNG GGTTGCTTNT GCNAGAGACG ATGATNATAN NTCGGAGCAC	420
	TGGCNTTTTC GACTANNAGT TTGACCGATG GCTATGTTCG TTTTGCTTTT CACCTTTTGT	480
30	CTTCCCATCT TTGCTGGTTC ACCTATGGAC GTTTGTTCCA TTTGGATGTN NTGAGAAATG	540
	CTGATGGCAT TTTCGGAAAN AAAAANATNT AAAATCNCGA GAGTTCTTCT ANAGCGGCCG	600
525 525	CGGGCCCNTC NNTTTTCCCC CGGGTGGGGT ACCANGTTTG TTGTNCCCNT TCCCCCTNTT	660
<b>4</b> 5	TGAGTCCTTT TACTNCCCCT GGCCGTCGTT TTATACNTCG TTGACTGGGA ANACCCTGCC	720
CT)	NT	722
40	(2) INFORMATION FOR SEQ ID NO: 9:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 793 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: unknown</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
50	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U131	
55	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 9:	
		•
60	GGCACGAGCC TTGCCCAACT CCTTCGATTC GTTCCAACGA TCGGAGAATG GCGCTGCTGG	60
~~	TGGAGAANAC GTCGACGGGA CGCGAGTACA AGGTGAAGGA CCTTTCTCAG GCTGACTTCG	120
	GCCGCCTCGA GATCGAGCTG GCGGAGGTGG AGATGCCGGG CCTCATGGCG TGCCGCGCCG	180
65	AGTTCGGGCC CGCCAAACCT TTCGCCGGCG CCCGCATCTC CGGCTCCCTC CACATGACCA	240
	TCCAGACCGC CGTCCTCATC GAGACCCTCA CCGCCCTCGG TGCTGAAGTC CGGTGGTGCT	300
	CCTGCAACAT CTTCTCCACC CAGGACCACG CCGCTGCCGC CATTGCCCGC GACTCCGCCG	360

CCGTCTTCGC CTGGAAGGGA GAGACCCTCG CCGAGTACTG GTGGTGCACC GAGCGATGCC